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SEQUENCE LISTING

(1) GENERAL INFORMATION

5

(i) APPLICANT: Tsichlis, Philip
Grimes, H. Leighton III
Zweidler-McKay, Patrick

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(ii) TITLE OF THE INVENTION: NUCLEIC ACID MOLECULE
FOR ENHANCING GENE EXPRESSION

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(iii) NUMBER OF SEQUENCES: 14

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(iv) CORRESPONDENCE ADDRESS:

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(A) ADDRESSEE: Dann, Dorfman, Herrell and
Skillman, P.C.
(B) STREET: 1601 Market Street, Suite 720
(C) CITY: Philadelphia
(D) STATE: Pennsylvania
(E) COUNTRY: USA
(F) ZIP: 19103-2307

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(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Diskette
(B) COMPUTER: IBM Compatible
(C) OPERATING SYSTEM: DOS
(D) SOFTWARE: FastSEQ Version 1.5

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(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: not assigned
(B) FILING DATE: 17-JUN-1997
(C) CLASSIFICATION:

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(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: US 60/019,808
(B) FILING DATE: 17-JUN-1996

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(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Janet E. Reed
(B) REGISTRATION NUMBER: 36,252
(C) REFERENCE/DOCKET NUMBER:

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(ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: (215) 563-4100
(B) TELEFAX: (215) 563-4044
(C) TELEX:

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(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 12 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

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(ii) MOLECULE TYPE: cDNA
(iii) HYPOTHETICAL: NO
(iv) ANTISENSE: NO
(v) FRAGMENT TYPE:
5 (vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

10 NAAATCACNG CA
12

(2) INFORMATION FOR SEQ ID NO:2:

15 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 12 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

20 (ii) MOLECULE TYPE: cDNA
(iii) HYPOTHETICAL: NO
(iv) ANTISENSE: NO
(v) FRAGMENT TYPE:
25 (vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

30 TAAATCACNG CA
32

(2) INFORMATION FOR SEQ ID NO:3:

35 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 12 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

40 (ii) MOLECULE TYPE: cDNA
(iii) HYPOTHETICAL: NO
(iv) ANTISENSE: NO
(v) FRAGMENT TYPE:
45 (vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

50 NANNNNACNG CA
52

(2) INFORMATION FOR SEQ ID NO:4:

55 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 24 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

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(iii) MOLECULE TYPE: cDNA
(iii) HYPOTHETICAL: NO
(iv) ANTISENSE: NO
(v) FRAGMENT TYPE:
5 (vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

ANAAAANAAA TCACNGCATA TGCC
10 24

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:
15 (A) LENGTH: 33 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

20 (ii) MOLECULE TYPE: cDNA
(iii) HYPOTHETICAL: NO
(iv) ANTISENSE: NO
(v) FRAGMENT TYPE:
25 (vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

ACCATCACCA CATAAATCAC TGCCTATCCT GTG
30 33

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:
35 (A) LENGTH: 24 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

40 (ii) MOLECULE TYPE: cDNA
(iii) HYPOTHETICAL: NO
(iv) ANTISENSE: NO
(v) FRAGMENT TYPE:
45 (vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

CACCACATAA ATCACTGCCT ATCC
50 24

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:
55 (A) LENGTH: 24 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

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(ii) MOLECULE TYPE: cDNA
(iii) HYPOTHETICAL: NO
(iv) ANTISENSE: NO
(v) FRAGMENT TYPE:
5 (vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

10 CACCA~~C~~CATAG ATCACTGCCT ATCC
24

(2) INFORMATION FOR SEQ ID NO:8:

15 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 24 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

20 (ii) MOLECULE TYPE: cDNA
(iii) HYPOTHETICAL: NO
(iv) ANTISENSE: NO
(v) FRAGMENT TYPE:
25 (vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

30 CACCA~~C~~CATAA CTCACTGCCT ATCC
24

(2) INFORMATION FOR SEQ ID NO:9:

35 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 24 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

40 (ii) MOLECULE TYPE: cDNA
(iii) HYPOTHETICAL: NO
(iv) ANTISENSE: NO
(v) FRAGMENT TYPE:
45 (vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

CACCA~~C~~CATAA ATA~~A~~CTGCCT ATCC
24

50 (2) INFORMATION FOR SEQ ID NO:10:

55 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 24 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

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- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTISENSE: NO
- (v) FRAGMENT TYPE:
- 5 (vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

10 CACCAACATAA ATCAATGCCT ATCC
24

(2) INFORMATION FOR SEQ ID NO:11:

- 15 (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 24 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- 20 (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTISENSE: NO
- (v) FRAGMENT TYPE:
- 25 (vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

CACCAACATAA ATCACTTCCT ATCC
30 24

(2) INFORMATION FOR SEQ ID NO:12:

- 35 (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 500 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- 40 (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTISENSE: NO
- (v) FRAGMENT TYPE:
- (vi) ORIGINAL SOURCE:

45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

50	GGCGGCCCTGG CTGACCGCCC AACGACCCCC CGGGATTGAC GTCAATAATG ACGTATGTTC	60
	CCATAGTAAC GCCAATAGGG ACTTTCCATT GACGTCAATG GGTGGAGTAT TTACGGTAAA	120
	CTGCCCACTT GGCAGTACAT CAAGTGTATC ATATGCAAG TACGCCCT ATTGACGTCA	180
	ATGACGGTAA ATGGCCGCC TGGCATTATG CCCAGTACAT GACCTTATGG GACTTCCCTA	240
	CTTGGCAGTA CATCTACGTA TTAGTCATCG CTATTACCAT GGTGATGCGG TTTTGGCAGT	300
	ACATCAATGG GCGTGGATAG CGGTTGACT CACGGGGATT TCCAAGTCTC CACCCCATG	360
	ACGTCATGG GAGTTGTTT TGGCACCAAATCAACGGGA CTTTCCAAAAA TGTCGTAACA	420
55	ACTCCGCCCC ATTGACGCAA ATGGGGGGTA GGCGTGTACG GTGGGAGGTC TATATAAGCA	480
	GAGCTCGTT AGTGAACCGT	500

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(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

5 (A) LENGTH: 500 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

10 (iii) HYPOTHETICAL: NO
 (iv) ANTISENSE: NO
 (v) FRAGMENT TYPE:
 (vi) ORIGINAL SOURCE:

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

GCCCCCCTGG	CTGACCGCCC	AACGACCCCC	CGGGATTGAC	GTCAATAATG	ACGTATGTTC	60
CCATAGTAAC	GCCAATAGGG	ACTTTCCATT	GACGTCAATG	GGTGGAGTAT	TTACCTAA	120
CTGCCCACTT	GGCAGTACAT	CAAGTGTATC	ATATGCCAAG	TACGCCCT	ATTGACGTCA	180
20 ATGACGGTAA	ATGGCCCCCC	TGGCATTATG	CCCACATACAT	GACCTTATGG	GACTTCCCTA	240
CTTGGCAGTA	CATCTACGTA	TTAGTCATCG	CTATTACCAT	GGTGATGCAG	TTTGCGCAGT	300
ACATCAATGG	GCGTGGATAG	CGGTTTGA	CACGGGAGT	TCCAAGTCTC	CACCCATTG	360
ACGTCATGG	GACTTTGTTT	TGGCACAAA	CTAACCGGA	CTTCCAAAAA	TGTCGTAACA	420
25 ACTCCGCCCC	ATTGACGCAA	ATGGCGGTA	GGCGTGTACG	GTGGGAGGTC	TATATAAGCA	480
GAGCTCGTTT	AGTGAACCGT					500

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

30 (A) LENGTH: 500 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

35 (iii) HYPOTHETICAL: NO
 (iv) ANTISENSE: NO
 (v) FRAGMENT TYPE:
 (vi) ORIGINAL SOURCE:

40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

GCCCCCCTGG	CTGACCGCCC	AACGACCCCC	CGGGATTGAC	GTCAATAATG	ACGTATGTTC	60
CCATAGTAAC	GCCAATAGGG	ACTTTCCATT	GACGTCAATG	GGTGGAGTAT	TTACGGTAA	120
45 CTGCCCACTT	GGCAGTACAT	CAAGTGTATC	ATATGCCAAG	TACGCCCT	ATTGACGTCA	180
ATGACGGTAA	ATGGCCCCCC	TGGCATTATG	CCCAGTACAT	GACCTTATGG	GACTTCCCTA	240
CTTGGCAGTA	CATCTACGTA	TTAGTCATCG	CTATTACCAT	GGTGATGCAG	TTTGCGCAGT	300
ACATCAATGG	GCGTGGATAG	CGGTTTGA	CACGGGACTT	TCCAAGTCTC	CACCCATTG	360
ACGTCATGG	GAGTTTGT	TGGCACAAA	ACTAACCGGA	CTTCCAAAAA	TGTCGTAACA	420
50 ACTCCGCCCC	ATTGACGCAA	ATGGCGGTA	GGCGTGTACG	GTGGGAGGTC	TATATAAGCA	480
GAGCTCGTTT	AGTGAACCGT					500